

Tzu Lip Phang, Ph.D.
Curriculum Vitae
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1. Current Position

Associate Professor of Bioinformatics
Division of Biomedical Informatics and Personalized Medicine
Department of Medicine
University of Colorado, Denver

Director, Translational Informatics Computational Resources (TICR)
Colorado Center for Personalized Medicine (CCPM)
University of Colorado, Department of Medicine

2. Education

Dates	Degree	University	Major
1991-1994	B.S.	University of Wyoming, Laramie	Chemistry
1994-1999	Ph.D.	University of Wyoming, Laramie	Molecular Biology
1999-2001	M.S.	University of Wyoming, Laramie	Computer Science
2001-2004	Post-Doc	University of Colorado, Denver	Bioinformatics

3. Academic Appointments

Dates	Position	Institution	Location
2004-2007	Research Associate	Department of Pharmacology University of Colorado	Aurora, Colorado
2007-2014	Assistant Professor (Primary Appointment)	Division of Pulmonary Sciences and Critical Care Medicine University of Colorado	Aurora, Colorado
2007-2014	Assistant Professor (Secondary Appointment)	School of Public Health University of Colorado	Aurora, Colorado
2007-2014	Assistant Professor (Secondary Appointment)	Computational Bioscience Program University of Colorado	Aurora, Colorado
2014-2016	Associate Professor	Division of Pulmonary Sciences and Critical Care Medicine University of Colorado	Aurora, Colorado

2014-current	Associate Professor (Secondary Appointment)	School of Public Health University of Colorado	Aurora, Colorado
2014-current	Associate Professor (Secondary Appointment)	Computational Bioscience Program University of Colorado	Aurora, Colorado
2016-current	Associate Professor	Division of Biomedical Informatics and Personalized Medicine University of Colorado	Aurora, Colorado

4. Membership in professional organizations

2001-current	Member, International Society for Computational Biology (ISCB)
2006-2017	co-director of Informatics Education Support, Colorado Clinical Translational Science Institute (CCTSI)
2006-2017	Analyst, Colorado Cancer Center

5. Major Committee and Service Responsibilities

2001-current	Member, International Society for Computational Biology (ISCB)
2006-2017	co-director of Informatics Education Support, Colorado Clinical Translational Science Institute (CCTSI)
2006-2017	Analyst, Colorado Cancer Center
2007-current	Computational BioScience Program (CPBS) teaching admission committee
2014-current	Co-director (founder) of biweekly Bioinformatics Journal Club
2017-current	Director, Translational Informatics and Computational Resources (TICR) for Colorado Center for Personalized Medicine (CCPM)
2017-current	Co-director (founder) of BioMedical Data Science (BMDS) Certificate Program

6. Inventions, intellectual property and patents held or pending

Invented the concept of **5X5**, where 5 scientific concepts were explained in 5 minutes. The idea was well received by the CTSI (Clinical Translational Science Initiative) nation wide and was implemented in Colorado CTSI Information Education website; <http://www.ucdenver.edu/research/CCTSI/programs-services/informatics/Pages/Informatics-Seminar-Learning-Tools-Archive.aspx>

Data Analysis Life Cycle: a novel approach to teach data analysis workflow. This course provides participants with hands-on experiences in solving real life biological problems using the Data Analysis Life Cycle approach; problem formulation, workflow design, trouble shooting, and scientific communication. Briefly, a Principal Investigator (PI) will be invited to describe a real life case study and formulate the analysis questions of interest. Next, the students will discuss and design different statistical analysis approach to address the questions, including trouble-shoot potential short falls. Lastly, students will perform a formal presentation on the analysis findings back to the PI. The novel course addresses a real gap in biomedical data analysis, namely facilitating a strong line of communication between biomedical researchers and data analysts. Excellent communication across disciplines is crucial, and failure to do so results in wasted time in many analysis projects

7. Review and referee work

- Software Review Section Editor: *Human Genomics Journal*
- Paper Reviewer: *Journal of Biomedical Informatics*, *PLoS Computational Biology*, *Environmental Molecular Sciences Laboratory*, *BMC Bioinformatics*, *Bioinformatics Journal*.

8. Invited extramural lectures, presentation and visiting professionships.

- Guest Lecture: *Microarray Data Analysis*, **BIOS 6659**, Sept, 2007
- Guest Moderator: *Systemic Onset Juvenile Idiopathic Arthritis (SoJIA)*, **Advance in Medical Science**, Mar, 2008
- Guest Lecture: *Connecting Lab Bench Sciences to the Public*, **HLTH 6071**, May, 2008
- Seminar Talk: *Microarray Analysis: Gene Expression Profiling and Beyond*, **Colorado Clinical Translational Science Institute (CCTSI) Monthly Seminar**, Mar, 2009
- Recurring Lecture: *Microarray Technology and Analysis*, CPBS 7711, **Fall Semester**
- Guest Lecture: *Reviewing Manuscripts*, **CPBS 7711**, Oct, 2010
- Guest Lecture: *Landscape of Bioinformatics Software for High-throughput Biological Data*, **BMGN 7620**, Mar, 2010
- Recurring Lecture: *Bioinformatics Tools in Context: How Informatics Improves Research Every Day*, **CLSC 7500**, Fall Semester
- Seminar Talk: *Bioinformatics of Transcriptome Analysis*, **Frontier in Pregnancy**, Sep, 2012
- Webiner Talk: *The "5X5" Program: Brief Videos for Informatics Education*, **CTSA Informatics Key Function Committee (IKFC)**, Feb, 2013
- Seminar Talk: *Unlocking The Potential of Public Available Gene Expression Data for Large-Scale Analysis*, **Bioinformatic Journal Club**, April, 2013
- Seminar Talk: *GEO2R: A Hands On Session On GEO Webtools to Analyze Publicly Available Gene Expression Microarray Dataset*, **Pulmonary Research Methods Conference**, May, 2013
- Seminar Talk: *Understanding Next Generation Sequencing Visualization Tools*, **Informatics Tools for Accelerating Clinical and Translational Research (IT-ACT)**, Sep 2013

- Seminar Talk: *Got Data? How to determine whether you need Bioinformatics and/or Biostatistics support for your research project*, **IT-ACT**, Jan, 2014
- Seminar Talk: *Power Analysis and Sample Size Estimation for RNA-Seq Differential Expression*, **Bioinformatics Journal Club**, Oct 2014
- Seminar Talk: *ChIP-seq Analysis of GR Binding in WT and KLF15 KO Mouse Embryonic Fibroblast*, **Lung System Biology Working Group**, Jan, 2015
- Seminar Talk: *Public dataset on Triple Negative Breast Cancer*, **DOD Breast Cancer quarterly meeting**, May, 2013

9. Teaching record

Courses

Dates	Course	Role
Fall 2008, Spring 2009 and Spring 2010	BIOS 6660: Microarray and High-throughput Data Analysis	Course Master
Summer 2008, 2009, 2010 and 2011	NHLBI, Genomic and Proteomic 10 Days Hands-On Workshop	Co-course Master
Fall 2009, 2010 and 2011	Initiative for Maximizing Student Diversity (IMSD): Introduction to Bioinformatics	Course Master
Spring 2011	CPBS 7792: Introduction to Human Phenotype	Co-course Master
Summer 2013	Colorado Biomedical Informatics Summer Training Fellowship	Program Director
Summer 2013, 2014, 2015, 2016, 2017	Annual AACR workshop at Snowmass CO: Molecular Biology in Clinical Oncology	Co-course Master
Spring 2014	Revamped BIOS6660: Analysis of Genomics Data Using R and Bioconductor (Data Analysis Life Cycle)	Course Master
Sep 2013 - June 2014	CCTSI Informatics Tools for Accelerating Clinical and Translational Research (IT-ACT) seminar series	Founder and host
Jan 2013 - current	AMC Bioinformatics Journal Club	Founder and host
Fall 2015	BIOS6660: Biomedical Big Data Analysis with R and BioConductor	Course Master
Fall 2016, 2017	BSBT6110: Introduction to Biocomputing	Course Master
Spring 2016, 2017	Bioinformatics Workshop at University of Zimbabwe	Co-course Master
Summer 2016, 2017	Colorado Summer Institute in Biostatistics (CoSIB)	Instructor

Presentations to students, trainees

Student Examination Committees

Date	Examination	Student
2009	Doctoral of Computational Bioscience Program	Todd Gibson
2010	Doctoral of Biostatistics, School of Public Health	Elizabeth Siewert
2014	Doctoral of Computational Bioscience Program	Daniel Dvorkin
2014	High-School Research Project: Winner: First Place Denver Molecular Biology Category (Intel Genius Award, Intel Excellence in Computer Science Award, Kristina R. Wenzel Memorial Award in Medicine)	Sirey Zhang
2016	Doctoral of Computational Bioscience Program	Charlotte Siska

10. Grant support

Current Funding

Title: The Colorado Summer Institute for Biostatistics (CoSIBS)

Funding Source: NIH/NHLBI

Role: Course Instructor

Completed Funding

Title: Functional Genomics to Identify miRNA Targets In The Developing Face

Funding Source: NIH/NIDCR

Role: co-Investigator

Title: Inflammation-Dependent Methylation In the Mucosa

Funding Source: NIH/NIDDK

Role: Data Analyst/Data Scientist

Title: Genetics of Alcohol Sensitivity in Rats

Funding Source: NIH/NHLBI

Role: Data Analyst/Data Scientist

Title: Colorado Clinical Translational Sciences Institute

Funding Source: NIH

Role: Data Analyst/Data Scientist

Title: Cancer Center Support Grant

Funding Source: NIH

Role: Bioinformatician

Title: Genotypic and Functional Properties Of HIV-1 Nef Clinical Isolates In PAH-HIV

Funding Source: NIH/NHLBI

Role: Data Analyst

Title: Androgen Receptors (AR) and Resistance to Current Endocrine Therapies: AR, Hypoxia, and the "Lipogenic Phenotype"

Funding Source: DOD

Role: Data Analyst

Title: Functional genomics of miRNAs in the developing face
Funding Source: NIH
Role: co-Investigator

Title: Functional Significance of Siglec-6, a novel leptin receptor, in human placental development and preeclampsia
Funding Source: NIH/NICHD
Role: Data Analyst

Title: Basal Cell-Specific Models: Identification of Tissue and Progenitor-Specific Genes
Funding Source: NIH
Role: Co-Investigator

Title: SPORE in Lung Cancer - Biostatistics and Informatics Core
Funding Source: NIH/NCI
Role: Bioinformatician

Title: Genetics of Alcohol Sensitivity in Rats
Funding Source: NIH/NIAAA
Role: Data Analyst

Title: Colorado Biomedical Informatics Training Program
Funding Source: NIH/NLM
Role: co-Investigator

Title: Lung Genomics Research Consortium
Funding Source: NIH/NHLBI
Role: Data Analyst

Title: IPAH Center for Genomics
Funding Source: CMREF
Role: Data Analyst

Title: Gene Expression Core
Funding Source: NCI
Role: Data Analyst

Title: Adaptations to Hypoxia
Funding Source: NIH/NHLBI
Role: Data Analyst

11. Bibliography

Peer-Reviewed Publications

1. Yoder, A.C., Guo, K., Dillon, S.M., Phang, T., Lee, E.J., Harper, M.S., Helm, K., Kappes, J.C., Ochsenbauer, C., McCarter, M.D., et al. (2017). The transcriptome of HIV-1 infected intestinal CD4+ T cells exposed to enteric bacteria. *PLoS Pathog* 13, e1006226.
2. Sasse, S.K., Kadiyala, V., Danhorn, T., Panettieri, R.A., Jr., Phang, T.L., and Gerber, A.N. (2017). Glucocorticoid Receptor ChIP-Seq Identifies PLCD1 as a KLF15 Target that Represses Airway Smooth Muscle Hypertrophy. *Am J Respir Cell Mol Biol* 57, 226-237.

3. Hooper, J.E., Feng, W., Li, H., Leach, S.M., Phang, T., Siska, C., Jones, K.L., Spritz, R.A., Hunter, L.E., and Williams, T. (2017). Systems biology of facial development: contributions of ectoderm and mesenchyme. *Dev Biol* 426, 97-114.
4. Kuokkanen, S., Polotsky, A.J., Chosich, J., Bradford, A.P., Jasinska, A., Phang, T., Santoro, N., and Appt, S.E. (2016). Corpus luteum as a novel target of weight changes that contribute to impaired female reproductive physiology and function. *Syst Biol Reprod Med* 62, 227-242.
5. Kadiyala, V., Sasse, S.K., Altonsy, M.O., Phang, T.L., and Gerber, A.N. (2016). Cistrome Analysis of Glucocorticoid Receptor Activity in Bronchial Epithelial Cells Defines Novel Mechanisms of Steroid Efficacy. *Ann Am Thorac Soc* 13 Suppl 1, S103.
6. Kadiyala, V., Sasse, S.K., Altonsy, M.O., Berman, R., Chu, H.W., Phang, T.L., and Gerber, A.N. (2016). Cistrome-based Cooperation between Airway Epithelial Glucocorticoid Receptor and NF-kappaB Orchestrates Anti-inflammatory Effects. *J Biol Chem* 291, 12673-12687.
7. Walter, N.D., Miller, M.A., Vasquez, J., Weiner, M., Chapman, A., Engle, M., Higgins, M., Quinones, A.M., Roselli, V., Canono, E., et al. (2015). Blood transcriptional biomarkers for active TB among US patients: A case-control study with systematic cross-classifier evaluation. *J Clin Microbiol*.
8. Sasse, S.K., Zuo, Z., Kadiyala, V., Zhang, L., Pufall, M.A., Jain, M.K., Phang, T.L., Stormo, G.D., and Gerber, A.N. (2015). Response Element Composition Governs Correlations between Binding Site Affinity and Transcription in Glucocorticoid Receptor Feed-forward Loops. *J Biol Chem* 290, 19756-19769.
9. Merhi, Z., Polotsky, A.J., Bradford, A.P., Buyuk, E., Chosich, J., Phang, T., Jindal, S., and Santoro, N. (2015). Adiposity Alters Genes Important in Inflammation and Cell Cycle Division in Human Cumulus Granulosa Cell. *Reprod Sci* 22, 1220-1228.
10. Green, R.M., Feng, W., Phang, T., Fish, J.L., Li, H., Spritz, R.A., Marcucio, R.S., Hooper, J., Jamniczky, H., Hallgrimsson, B., et al. (2015). Tfp2a-dependent changes in mouse facial morphology result in clefting that can be ameliorated by a reduction in Fgf8 gene dosage. *Dis Model Mech* 8, 31-43.
11. Baumgartner, H.K., Trinder, K.M., Galimanis, C.E., Post, A., Phang, T., Ross, R.G., and Winn, V.D. (2015). Characterization of choline transporters in the human placenta over gestation. *Placenta* 36, 1362-1369.
12. Al-Safi, Z.A., Liu, H., Carlson, N.E., Chosich, J., Lesh, J., Robledo, C., Bradford, A.P., Gee, N.A., Phang, T., Santoro, N., et al. (2015). Estradiol Priming Improves Gonadotrope Sensitivity and Pro-inflammatory Cytokines in Obese Women. *J Clin Endocrinol Metab*, jc20151946.
13. Altonsy, M.O., Sasse, S.K., Phang, T.L., and Gerber, A.N. (2014). Context-dependent cooperation between nuclear factor kappaB (NF-kappaB) and the glucocorticoid receptor at a TNFAIP3 intronic enhancer: a mechanism to maintain negative feedback control of inflammation. *J Biol Chem* 289, 8231-8239.
14. Reisdorph, N., Stearman, R., Kechris, K., Phang, T.L., Reisdorph, R., Prenni, J., Erle, D.J., Coldren, C., Schey, K., Nesvizhskii, A., et al. (2013). Hands-on workshops as an effective means of learning advanced technologies including genomics, proteomics and bioinformatics. *Genomics Proteomics Bioinformatics* 11, 368-377.
15. Frantz, A.M., Sarver, A.L., Ito, D., Phang, T.L., Karimpour-Fard, A., Scott, M.C., Valli, V.E., Lindblad-Toh, K., Burgess, K.E., Husbands, B.D., et al. (2013). Molecular Profiling Reveals Prognostically Significant Subtypes of Canine Lymphoma. *Vet Pathol*.
16. Darlington, T.M., Ehringer, M.A., Larson, C., Phang, T.L., and Radcliffe, R.A. (2013). Transcriptome analysis of Inbred Long Sleep and Inbred Short Sleep mice. *Genes Brain Behav* 12, 263-274.
17. Wang, J., Nikrad, M.P., Travanty, E.A., Zhou, B., Phang, T., Gao, B., Alford, T., Ito, Y., Nahreini, P., Hartshorn, K., et al. (2012). Innate immune response of human alveolar macrophages during influenza A infection. *Plos One* 7, e29879.

18. Shaw, L.A., Stefanski, A.L., Peterson, L.K., Rumer, K.K., Vondracek, A., Phang, T.L., Sakaguchi, S., Winn, V.D., and Dragone, L.L. (2012). Pregnancy amelioration of arthritis in SKG mice corresponds with alterations in serum amyloid A3 levels. *Am J Clin Exp Immunol* 1, 12-19.
19. Kiseljak-Vassiliades, K., Shafi, S., Kerr, J.M., Phang, T.L., Kleinschmidt-Demasters, B.K., and Wierman, M.E. (2012). Clinical implications of growth hormone-secreting tumor subtypes. *Endocrine* 42, 18-28.
20. Clark, D.W., Phang, T., Edwards, M.G., Geraci, M.W., and Gillespie, M.N. (2012). Promoter G-quadruplex sequences are targets for base oxidation and strand cleavage during hypoxia-induced transcription. *Free Radic Biol Med* 53, 51-59.
21. Wang, J.R., Nikrad, M.P., Phang, T., Gao, B.F., Alford, T., Ito, Y., Edeen, K., Travanty, E.A., Kosmider, B., Hartshorn, K., et al. (2011). Innate Immune Response to Influenza A Virus in Differentiated Human Alveolar Type II Cells. *Am J Resp Cell Mol* 45, 582-591.
22. Phang, T.L., Zeng, P.Y., and de Zoeten, E.F. (2011). Exploring and Profiling Long Non-coding RNA in T cell Development Using Next Generation Sequencing and Bioinformatics approaches. In *Annual Rocky Mountain Bioinformatics Conference*. (Snowmass, CO).
23. Phang, T.L., Feng, W., Radcliffe, R.A., and Kechris, K. (2011). Post-processing multi-treatment time-course microarray studies using the Johnson-Neyman procedure. *Biostatistics, Bioinformatics and Biomathematics* 2, 107-126.
24. Olincy, A., House, R., Gao, B., Recksiek, P., Phang, T.L., Sullivan, B., Hollis, J.P., Hopkins, J., Shade, T., Edwards, M.G., et al. (2011). Elevated DISC1 transcript levels in PBMCs during acute psychosis in patients with schizophrenia. *Transl Biomed* 2.
25. Kim, H., Kim, J., Selby, H., Gao, D., Tong, T., Phang, T.L., and Tan, A.C. (2011). A short survey of computational analysis methods in analysing ChIP-seq data. *Hum Genomics* 5, 117-123.
26. Burnham, E.L., Phang, T.L., House, R., Vandivier, R.W., Moss, M., and Gaydos, J. (2011). Alveolar Macrophage Gene Expression Is Altered in the Setting of Alcohol Use Disorders. *Alcohol Clin Exp Res* 35, 284-294.
27. Tyler, K.L., Leser, J.S., Phang, T.L., and Clarke, P. (2010). Gene expression in the brain during reovirus encephalitis. *J Neurovirol* 16, 56-71.
28. Tamburini, B.A., Phang, T.L., Fosmire, S.P., Scott, M.C., Trapp, S.C., Duckett, M.M., Robinson, S.R., Slansky, J.E., Sharkey, L.C., Cutter, G.R., et al. (2010). Gene expression profiling identifies inflammation and angiogenesis as distinguishing features of canine hemangiosarcoma. *Bmc Cancer* 10.
29. Phang, T.L., Kim, H., Kim, J., Gao, D., Tong, T., Selby, H., and Tan, A.C. (2010). AN ANALYSIS WORKFLOW FOR LOSS-OF-FUNCTION RNA INTERFERENCE WHOLE-GENOME SCREENING USING THE NEXT GENERATION SEQUENCING TECHNOLOGY. In *Aspen Lung Conference*. (Aspen, CO).
30. Phang, T.L., Kim, H., Kim, J., Gao, D., Tong, T., Selby, H., Gregory, M.A., DeGregori, J., and Tan, A.C. (2010). BiNGS!SL-Seq: A Computational Analysis Workflow for Whole-Genome RNA Interference Screening Using the Next Generation Sequencing Technology. In *Intelligent Systems for Molecular Biology*. (Boston, MA).
31. Phang, T.L., Hunter, A., Zeng, P.Y., Kerbowski, T., and de Zoeten, E.F. (2010). Analysis workflow of Methylation and Gene Expression microarray in Pediatric Crohn Disease. In *Annual Rocky Mountain Bioinformatics Conference*. (Snowmass, CO).
32. Karimpour-Fard, A., Dumas, L., Phang, T., Sikela, J.M., and Hunter, L.E. (2010). A survey of analysis software for array-comparative genomic hybridisation studies to detect copy number variation. *Hum Genomics* 4, 421-427.
33. Gregory, M.A., Phang, T.L., Neviani, P., Alvarez-Calderon, F., Eide, C.A., O'Hare, T., Zaberezhnyy, V., Williams, R.T., Druker, B.J., Perrotti, D., et al. (2010). Wnt/Ca2+/NFAT Signaling Maintains Survival of Ph+ Leukemia Cells upon Inhibition of Bcr-Abl. *Cancer Cell* 18, 74-87.

34. Gao, D., Kim, J., Kim, H., Phang, T.L., Selby, H., Tan, A.C., and Tong, T. (2010). A survey of statistical software for analysing RNA-seq data. *Hum Genomics* 5, 56-60.
35. Calverley, D.C., Phang, T.L., Choudhury, Q.G., Gao, B., Oton, A.B., Weyant, M.J., and Geraci, M.W. (2010). Significant downregulation of platelet gene expression in metastatic lung cancer. *Clin Transl Sci* 3, 227-232.
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37. Woo, D.K., Phang, T.L., Trawick, J.D., and Poyton, R.O. (2009). Multiple pathways of mitochondrial-nuclear communication in yeast: Intergenomic signaling involves ABF1 and affects a different set of genes than retrograde regulation. *Bba-Gene Regul Mech* 1789, 135-145.
38. Winn, V.D., Shaw, L., Rumer, K.K., Kramer, A., Sakaguchi, S., and Dragone, L.L. (2009). Pregnancy-Induced Rheumatoid Arthritis (RA) Amelioration in SKG Mice. *Reprod Sci* 16, 83A-83A.
39. Tamburini, B.A., Trapp, S., Phang, T.L., Schappa, J.T., Hunter, L.E., and Modiano, J.F. (2009). Gene Expression Profiles of Sporadic Canine Hemangiosarcoma Are Uniquely Associated with Breed. *Plos One* 4.
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42. Feng, W.G., Leach, S.M., Tipney, H., Phang, T., Geraci, M., Spritz, R.A., Hunter, L.E., and Williams, T. (2009). Spatial and Temporal Analysis of Gene Expression during Growth and Fusion of the Mouse Facial Prominences. *Plos One* 4.
43. Harvell, D.M., Spoelstra, N.S., Singh, M., McManaman, J.L., Finlayson, C., Phang, T., Trapp, S., Hunter, L., Dye, W.W., Borges, V.F., et al. (2008). Molecular signatures of neoadjuvant endocrine therapy for breast cancer: characteristics of response or intrinsic resistance. *Breast Cancer Res Treat* 112, 475-488.
44. Rudolph, M.C., McManaman, J.L., Phang, T., Russell, T., Kominsky, D.J., Serkova, N.J., Stein, T., Anderson, S.M., and Neville, M.C. (2007). Metabolic regulation in the lactating mammary gland: a lipid synthesizing machine. *Physiol Genomics* 28, 323-336.
45. Bhave, S.V., Hornbaker, C., Phang, T.L., Saba, L., Lapadat, R., Kechris, K., Gaydos, J., McGoldrick, D., Dolbey, A., Leach, S., et al. (2007). The PhenoGen informatics website: tools for analyses of complex traits. *BMC Genet* 8, 59.
46. Guzelian, J., Barwick, J.L., Hunter, L., Phang, T.L., Quattrochi, L.C., and Guzelian, P.S. (2006). Identification of genes controlled by the pregnane X receptor by microarray analysis of mRNAs from pregnenolone 16alpha-carbonitrile-treated rats. *Toxicol Sci* 94, 379-387.
47. Shenkar, R., Elliott, J.P., Diener, K., Gault, J., Hu, L.J., Cohrs, R.J., Phang, T., Hunter, L., Breeze, R.E., and Awad, I.A. (2003). Differential gene expression in human cerebrovascular malformations. *Neurosurgery* 52, 465-477; discussion 477-468.
48. Rudolph, M.C., McManaman, J.L., Hunter, L., Phang, T., and Neville, M.C. (2003). Functional development of the mammary gland: Use of expression profiling and trajectory clustering to reveal changes in gene expression during pregnancy, lactation, and involution. *J Mammary Gland Biol* 8, 287-307.
49. Phang, T.L., Neville, M.C., Rudolph, M., and Hunter, L. (2003). Trajectory clustering: a non-parametric method for grouping gene expression time courses, with applications to mammary development. *Pac Symp Biocomput*, 351-362.

50. Lewis, G.S., Jewell, J.E., Phang, T., and Miller, K.W. (2003). Mutational and sequence analysis of transmembrane segment 6 orientation in TetA proteins. *Biochem Biophys Res Commun* 305, 1067-1072.
51. Hoshikawa, Y., Nana-Sinkam, P., Moore, M.D., Sotto-Santiago, S., Phang, T., Keith, R.L., Morris, K.G., Kondo, T., Tuder, R.M., Voelkel, N.F., et al. (2003). Hypoxia induces different genes in the lungs of rats compared with mice. *Physiol Genomics* 12, 209-219.
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56. Hong, S.H., Phang, T., Ji, I.H., and Ji, T.H. (1998). The amino-terminal region of the luteinizing hormone choriogonadotropin receptor contacts both subunits of human choriogonadotropin I. Mutational analysis. *J Biol Chem* 273, 13835-13840.
57. Phang, T.L., Ji, I.H., and Ji, T.H. (1996). No need of acetic acid for processing polyacrylamide gels. *Anal Biochem* 234, 96-97.
58. Ji, I., Pan, Y.N., Lee, Y.M., Phang, T., and Ji, T.H. (1995). Receptor binding dependent structural changes in human choriogonadotropin: photochemical inter-subunit crosslinking. *Endocrine* 3, 907-911.

Scientific abstracts published or presented at scientific meeting:

1. **Phang TL**, Neville MC, Rudolph M, and Hunter L. Trajectory Clustering: a Non-Parametric Method for Grouping Gene Expression Time Courses, with Applications to Mammary Development. *In: Pacific Symposium in Biocomputing, Jan 3-7 2003; Lihue, Hawaii*
2. **Phang TL**. Swimming in the sea of class prediction software tools for microarray expression data analysis. *In: High Technology Approaches to Gender-Specific Disease Symposium, Oct 5 2006; Denver, CO*
3. **Phang TL**, Feng W, Radcliffe RA, Kechris K. A semi-manual method using the ANCOVA framework to identify expression profiles in time-course microarray experiments. *In: Annual Rocky Mountain Bioinformatics Conference: Nov 30 - Dec 2 2007; Snowmass, CO.*
4. **Phang TL**, Hunter A, Zeng PY, Kerbowski T, de Zoeten EF: Analysis workflow of Methylation and Gene Expression microarray in Pediatric Crohn Disease. *In: Annual Rocky Mountain Bioinformatics Conference: Dec 9-11 2010; Snowmass, CO.*
5. **Phang TL**, Kim H, Kim J, Gao D, Tong T, Selby H, Gregory MA, DeGregori J, Tan AC: BiNGS!SL-Seq: A Computational Analysis Workflow for Whole-Genome RNA Interference Screening Using the Next Generation Sequencing Technology. *In: Intelligent Systems for Molecular Biology: July 11-13 2010; Boston, MA.*

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Software

- Trajectory Clustering: a novel clustering algorithm to group time-course microarray data [10]
- Formal manager and developer of the PhenoGen Informatics Website (<http://phenogen.ucdenver.edu/PhenoGen/>) [14]
- Developed R and Bioconductor Statistical Analysis Pipelines:
 - Gene Expression, Copy-Number, and MicroRNA Microarray Data Analysis
 - shRNA synthetic lethality assay data analysis
 - Long non-coding RNA expression analysis pipeline
 - Alternative Splicing Analysis
 - Transcriptomic (RNA-seq) Next Generation Sequencing (NGS) Data Analysis
 - Whole Exome (Exome-seq) NGS Data Analysis
 - Chromatin Immunoprecipitation Sequencing (ChIP-seq) NGS Data Analysis

Book Scientific Illustration

I am an amateur illustrator and motivated to contribute to sciences via graphical representation. I have helped many collaborators generate publication ready figures [36,37]. I had an opportunity to illustrate Dr. Larry Hunter's textbook, titled "The Processes of Life" (MIT Press, ISBN-13: 978-0262013055), and thoroughly enjoyed the experience